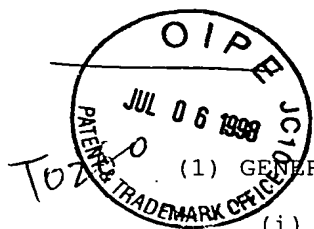


SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANT: Radosevich, James A.
- (ii) TITLE OF INVENTION: A GENE ENCODING A NOVEL MARKER FOR CANCER
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
 - (B) STREET: NBC Tower - Suite 3600, 455 N. Cityfront Plaza Drive
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: USA
 - (F) ZIP: 60611-5599
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/040,485
 - (B) FILING DATE: 17-MAR-1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Martin, Alice O.
 - (B) REGISTRATION NUMBER: 35,601
 - (C) REFERENCE/DOCKET NUMBER: 8998/3
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 312-321-4200
 - (B) TELEFAX: 312-321-4299

RECEIVED
JUL 17 1998
GROUP 1800

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 70..834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGGAGCTTG AAGGACACAA GAATGGGAGG AAAGGCGGAC TCTCAGGAAC TTCATTCTTC

60

ACGTGGTTT	ATG	GTG	ATT	GCA	TTG	CTG	GGC	GTC	TGG	ACA	TCT	GTA	GCT		108
	Met	Val	Ile	Ala	Leu	Leu	Gly	Val	Trp	Thr	Ser	Val	Ala		
	1				5				10						
GTC	GTT	TGG	TTT	GAT	CTT	GTT	GAC	TAT	GAG	GAA	GTT	CTA	GGA	AAA	CTA
Val	Val	Trp	Phe	Asp	Leu	Val	Asp	Tyr	Glu	Glu	Val	Leu	Gly	Lys	Leu
	15				20				25						
GGA	ATC	TAT	GAT	GCT	GAT	GGT	GAT	GGA	GAT	TTT	GAT	GTG	GAT	GAT	GCC
Gly	Ile	Tyr	Asp	Ala	Asp	Gly	Asp	Gly	Asp	Phe	Asp	Val	Asp	Asp	Ala
	30				35				40						45
AAA	GTT	TTA	TTA	GGA	CTT	AAA	GAG	AGA	TCT	ACT	TCA	GAG	CCA	GCA	GTC
Lys	Val	Leu	Leu	Gly	Leu	Lys	Glu	Arg	Ser	Thr	Ser	Glu	Pro	Ala	Val
				50					55					60	
CCG	CCA	GAA	GAG	GCT	GAG	CCA	CAC	ACT	GAG	CCC	GAG	GAG	CAG	GTT	CCT
Pro	Pro	Glu	Glu	Ala	Glu	Pro	His	Thr	Glu	Pro	Glu	Glu	Gln	Val	Pro
			65					70					75		
GTG	GAG	GCA	GAA	CCC	CAG	AAT	ATC	GAA	GAT	GAA	GCA	AAA	GAA	CAA	ATT
Val	Glu	Ala	Glu	Pro	Gln	Asn	Ile	Glu	Asp	Glu	Ala	Lys	Glu	Gln	Ile
		80					85					90			
CAG	TCC	CTT	CTC	CAT	GAA	ATG	GTA	CAC	GCA	GAA	CAT	GTT	GAG	GGA	GAA
Gln	Ser	Leu	Leu	His	Glu	Met	Val	His	Ala	Glu	His	Val	Glu	Gly	Glu
	95					100					105				
GAC	TTG	CAA	CAA	GAA	GAT	GGA	CCC	ACA	GGA	GAA	CCA	CAA	CAA	GAG	GAT
Asp	Leu	Gln	Gln	Glu	Asp	Gly	Pro	Thr	Gly	Glu	Pro	Gln	Gln	Glu	Asp
	110				115				120						125
GAT	GAG	TTT	CTT	ATG	GCG	ACT	GAT	GTA	GAT	GAT	AGA	TTT	GAG	ACC	CTG
Asp	Glu	Phe	Leu	Met	Ala	Thr	Asp	Val	Asp	Asp	Arg	Phe	Glu	Thr	Leu
			130						135					140	
GAA	CCT	GAA	GTA	TCT	CAT	GAA	GAA	ACC	GAG	CAT	AGT	TAC	CAC	GTG	GAA
Glu	Pro	Glu	Val	Ser	His	Glu	Glu	Thr	Glu	His	Ser	Tyr	His	Val	Glu
			145					150					155		
GAG	ACA	GTT	TCA	CAA	GAC	TGT	AAT	CAG	GAT	ATG	GAA	GAG	ATG	ATG	TCT
Glu	Thr	Val	Ser	Gln	Asp	Cys	Asn	Gln	Asp	Met	Glu	Glu	Met	Met	Ser
		160					165					170			
GAG	CAG	GAA	AAT	CCA	GAT	TCC	AGT	GAA	CCA	GTA	GTA	GAA	GAT	GAA	AGA
Glu	Gln	Glu	Asn	Pro	Asp	Ser	Ser	Glu	Pro	Val	Val	Glu	Asp	Glu	Arg
		175				180					185				
TTG	CAC	CAT	GAT	ACA	GAT	GAT	GTA	ACA	TAC	CAA	GTC	TAT	GAG	GAA	CAA
Leu	His	His	Asp	Thr	Asp	Asp	Val	Thr	Tyr	Gln	Val	Tyr	Glu	Glu	Gln
	190				195				200						205
GCA	GTA	TAT	GAA	CCT	CTA	GAA	AAT	GAA	GGG	ATA	GAA	ATC	ACA	GAA	GTA
Ala	Val	Tyr	Glu	Pro	Leu	Glu	Asn	Glu	Gly	Ile	Glu	Ile	Thr	Glu	Val
				210					215					220	
ACT	GCT	CCC	CCT	GAG	GAT	AAT	CCT	GTA	GAA	GAT	TCA	CAG	GTA	ATT	GTA
Thr	Ala	Pro	Pro	Glu	Asp	Asn	Pro	Val	Glu	Asp	Ser	Gln	Val	Ile	Val
			225					230					235		

GAA GAA GTA AGC ATT TTT CCT GTG GAA GAA CAG CAG GAA GTA CCA CCA	828
Glu Glu Val Ser Ile Phe Pro Val Glu Glu Gln Gln Glu Val Pro Pro	
240 245 250	
GAT ACT TAAAGCTTCA AAAAGACTGC CCCTACCACC ACAGGAGGAC CAGCCTAACC	884
Asp Thr	
255	
ATACGCTCCA AAAGATGGCT GTGATAGATC TTGTGAAGCA ATTACTGAGC AGATCAAGAT	944
CTTTGGGAAG GAACACTAAA GATGTTTTGA ATGAATTATA GTCCACTGGC ATTTTAGTGT	1004
ATTTTTTTTT CTTTTTAGAA ACACACATTT CTAAAAATGT CATGTTACAT TCCTGCATGT	1064
CCCTTTTGAT AGCATTAGTG GATCCATTGG ATTTCTTTTT TCTTTTTGTG AGACAGCTTT	1124
TAGTCTTACC TGAATTTATG TGTGTTTTTC CGACAGTGGT TAATAATTAT ATTGGTGATG	1184
TAGCAGCAAT TGTGTTGGCA GGGTTTTTCAT ATATTATTAG TAATTAACAC TAACTGTTGG	1244
ACTGACTTGT GTACACTGTG TTAAACATGA TTTAAAAGCT ATTAAGAGTA CTTTGTGTTA	1304
GCACTCTTAA AAACGCTAAC AGAGATCATC ATTAGCTGTG AAGATTTGAG TTGTATATAC	1364
CTGCACTGAT ATTCTTATCA AAAATTTCTA CATTAGCTTT AAGTGTTTCTAG ATTAACACTT	1424
TTGAAACCTT TGTAGCTTTT AGCTGATTAA TTAGAAAAAT TAATATTTCA GTGAAAGTTT	1484
TAAATTATCA TTTATTTATT TTTTAAATG AGAGGGGAAA GCTGAAATTC CTTGTTAAGA	1544
CACAAGGAAA AAGAATGGCC CTACTATTAT CATGCAAAAA TGCTTTGTTG GCACCTCAGA	1604
TTAATCATAT AATAGCTATA GTCTCTTCAG CATTTGTTTA AATTTTAGAA AACCTGTATA	1664
AATTACTGGT GCATAACTTA AAGATTATTC TGCCTTTGGC TAATTGAGTA ATTCCCCTCC	1724
AGCACTAGAG ACCGCTCAGT GCTCTTACTA GATGAACTCA GTAACGCCTT GAGCTGGGTT	1784
GATTGAGGAT GTGTGAAAAA GCTCACAGAG CCCGATGCCT GCTGCTATTT CACGGCAATG	1844
AGCCTTTTTT TTTCTACACT GAAGATTTTC TTCTTATTTA ATGTGGTTTA TTTTGGGCTC	1904
AGAAATAATT GCTCTGTTGA AAATAATCCT TTGTCAGAAA AGAAGGTAGC TACCACATCA	1964
TTTTGAAAGG ACCATGAGCA ACTATAAGCA AAGCCATAAG AAGTGGTTTG ATCGATATAT	2024
TAGGGGTAGC TCTTGATTTT GTTAACATTA AGATAAGGTG ACTTTTTCCC CCTGCTTTTA	2084
GGATTAAAAT CAAAGATACT TCTATATTTT TATCACTATA GATCATAGTT ATTATACAAT	2144
GTAGTGAGTC CTGCATGGGT ACTCGATGTG TAATGAAACC TGAAATAATA ATAAGATAAT	2204
AAGAAAAGCA ATAATTTTCT AAAGCTGTGC TGTCGGTGAT ACAGAGATGA TACTCAAATT	2264
ATAATAAAAC TCTTCATTTT GTGAATTATA GAAGCTACTT TTTATAAAGC CATATTTTTT	2324
TAGGGAAACT AAGGAGTGAC ATAGAAGTGA TGAATGAGTA AAAGTAAGTT TTGCTGGATT	2384
TTTGTAGAAC TCTGGACGTT GAGGATTCAT TATGCTGTGG TTAACTTTAA ATATTTTT	2442

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Val	Ile	Ala	Leu	Leu	Gly	Val	Trp	Thr	Ser	Val	Ala	Val	Val	Trp
1				5				10						15	
Phe	Asp	Leu	Val	Asp	Tyr	Glu	Glu	Val	Leu	Gly	Lys	Leu	Gly	Ile	Tyr
			20					25					30		
Asp	Ala	Asp	Gly	Asp	Gly	Asp	Phe	Asp	Val	Asp	Asp	Ala	Lys	Val	Leu
			35				40					45			
Leu	Gly	Leu	Lys	Glu	Arg	Ser	Thr	Ser	Glu	Pro	Ala	Val	Pro	Pro	Glu
	50					55					60				
Glu	Ala	Glu	Pro	His	Thr	Glu	Pro	Glu	Glu	Gln	Val	Pro	Val	Glu	Ala
	65				70					75					80
Glu	Pro	Gln	Asn	Ile	Glu	Asp	Glu	Ala	Lys	Glu	Gln	Ile	Gln	Ser	Leu
				85					90					95	
Leu	His	Glu	Met	Val	His	Ala	Glu	His	Val	Glu	Gly	Glu	Asp	Leu	Gln
			100					105					110		
Gln	Glu	Asp	Gly	Pro	Thr	Gly	Glu	Pro	Gln	Gln	Glu	Asp	Asp	Glu	Phe
			115				120					125			
Leu	Met	Ala	Thr	Asp	Val	Asp	Asp	Arg	Phe	Glu	Thr	Leu	Glu	Pro	Glu
			130				135				140				
Val	Ser	His	Glu	Glu	Thr	Glu	His	Ser	Tyr	His	Val	Glu	Glu	Thr	Val
	145				150					155					160
Ser	Gln	Asp	Cys	Asn	Gln	Asp	Met	Glu	Glu	Met	Met	Ser	Glu	Gln	Glu
				165					170					175	
Asn	Pro	Asp	Ser	Ser	Glu	Pro	Val	Val	Glu	Asp	Glu	Arg	Leu	His	His
			180					185					190		
Asp	Thr	Asp	Asp	Val	Thr	Tyr	Gln	Val	Tyr	Glu	Glu	Gln	Ala	Val	Tyr
			195				200					205			
Glu	Pro	Leu	Glu	Asn	Glu	Gly	Ile	Glu	Ile	Thr	Glu	Val	Thr	Ala	Pro
	210					215					220				
Pro	Glu	Asp	Asn	Pro	Val	Glu	Asp	Ser	Gln	Val	Ile	Val	Glu	Glu	Val
	225				230					235					240
Ser	Ile	Phe	Pro	Val	Glu	Glu	Gln	Gln	Glu	Val	Pro	Pro	Asp	Thr	
				245					250					255	

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val Lys Lys Ala Phe Ala Ile Ile Asp Gln Asp Lys Ser Gly Phe Ile
 1 5 10 15

Glu Glu Asp Glu Leu Lys Leu Phe Leu Gln Asn Phe
 20 25

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Ala Gly Asp Gly Thr Ile
 1 5 10 15

Thr Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu
 20 25

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Leu Ala Asp Cys Phe Arg Val Phe Asp Lys Asn Ala Asp Gly Phe Ile
 1 5 10 15

Asp Ile Glu Glu Leu Gly Glu Ile Leu Arg Ala Thr
 20 25

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Pro Pro Glu Asp Asn Pro Val Glu Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Glu Glu Gln Gln Glu Val Pro Pro Asp Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Gly Pro Thr Gly Glu Pro Gln Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gln Glu Asn Pro Asp Ser Ser Glu Pro Val
1 5 10
